Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-109. (canceled)

110. (currently amended) A ~~thermodynamic~~ method for ~~predicting duplex stability of~~ designing an oligonucleotide sequence having a selected duplex stability ~~comprising at least one modified nucleotide base, said method~~ comprising:

a) providing an oligonucleotide having a sequence of N bases and N-1 neighboring base pairs, wherein said oligonucleotide comprises at least one modified base selected from the group consisting of a universal base, unsubstituted and 3-substituted pyrazolo[3,4-d]pyrimidines and unsubstituted and 5-substituted pyrimidines; and

b) calculating the duplex stability of said oligonucleotide using an algorithm applying a nearest-neighbor model for duplex formation thermodynamics for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases, optionally repeating steps a)-b) to obtain a sequence having said selected duplex stability.

111. (currently amended) A method for ~~predicting the melting temperature (T_m) of~~ designing an oligonucleotide sequence having a selected duplex stability ~~comprising at least one modified nucleotide base, said method~~ comprising:

a) providing an oligonucleotide having a sequence of N bases and N-1 neighboring base pairs, wherein said oligonucleotide comprises at least one modified base selected from the group consisting of a universal base, unsubstituted and 3-substituted pyrazolo[3,4-d]pyrimidines and unsubstituted and 5-substituted pyrimidines; and a minor groove binder; and

b) calculating a melting temperature (T_m) of said oligonucleotide using an algorithm applying nearest neighbor thermodynamic parameters for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases, optionally repeating steps a)-b) to obtain a sequence having said selected duplex stability.

112. (previously presented) The method of any one of claims **110** or **111**, wherein said oligonucleotide sequence is derived from a database source.

113. (currently amended) The method of claim **112**, wherein said ~~oligonucleotide sequence~~ database source is GENBANK ~~derived from Genbank~~.

114. (previously presented) The method of any one of claims **110** or **111**, wherein said at least one modified base is a member selected from the group consisting of a base attached to an amino acid, a polyamide nucleic acid (PNA) and a locked nucleic acid sugar.

115. (previously presented) The method of claim **114**, wherein said modified base is attached to PNA.

116. (currently amended) The method of claim **114**, wherein said modified base **is** a locked nucleic acid sugar.

117. (currently amended) The method of any one of claims **110** or **111**, wherein said oligonucleotide ~~comprising at least one modified base~~ has ~~superior~~ an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.

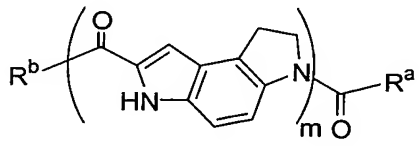
118. (previously presented) The method of any one of claims **110** or **111**, wherein said at least one modified base is a member selected from the group consisting of a

universal base, PPA, PPG, PPPA, PPPG, PU, PC, HOPU, HOBuU, HOBuC, $(NH_2)_2$PPPA, $(NH_2)_2$PPPAOH, $(NH_2)_2$BuPPAOH, $(NH_2)_2$PPAI, and HOBuPPG.

119. (currently amended) The method of claim ~~any one of claims~~ **110** ~~or 111~~, wherein said oligonucleotide has attached to it one or more members selected from the group consisting of a minor groove binder, a fluorophore and a quencher.

120. (previously presented) The method of claim **119**, wherein said oligonucleotide sequence has a minor groove binder attached thereto.

121. (currently amended) The method of claim **111** or **120**, wherein said minor groove binder has a formula selected from the group consisting of:



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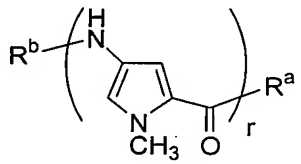
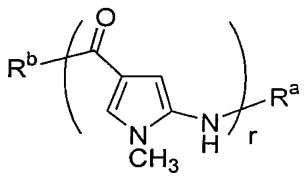


and


wherein

the subscript m is an integer of from 2 to 5;

the subscript r is an integer of from 2 to 10; and

each R^a and R^b is independently a linking group to said modified oligonucleotide, H, OR^c, NR^cR^d, $COOR^c$ and $-CONR^cR^d$ wherein each R^c and R^d is selected from the group consisting of H, $(C_1$-$C_{12})$heteroalkyl, $(C_2$-$C_{12})$heteroalkenyl, $(C_2$-$C_{12})$heteroalkynyl, $(C_1$-$C_{12})$alkyl, $(C_2$-$C_{12})$alkenyl, $(C_2$-$C_{12})$alkynyl, aryl$(C_1$-$C_{12})$alkyl and aryl.

122. (previously presented) The method of claim **120**, wherein said minor groove binder is attached to the oligonucleotide via a quencher molecule.

123. (previously presented) The method of any one of claims **110** or **111**, wherein said algorithm predicts the melting temperature (T_m) of said oligonucleotide with an accuracy of about +/- 2°C.

124. (currently amended) The method of any one of claims **110** or **111**, wherein said method is applied to establish ~~in establishing appropriate~~ conditions for hybridization, renaturation, mapping variations of base compositions of sequences or determination of sequence complexity and divergence.

125. (previously presented) The method of any one of claims **110** or **111**, wherein said oligonucleotide is a capture probe in an array.

126. (currently amended) The method of claim **115**, wherein said oligonucleotide ~~comprising at least one modified base~~ has ~~superior~~ an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.

127. (currently amended) The method of claim **116**, wherein said oligonucleotide ~~comprising at least one modified base~~ has ~~superior~~ an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.